Amendments to the Claims

Please amend claims 1, 3-17, and 31.

Please cancel claims 18-22.

The listing of claims will replace all prior versions, and listings of claims in the application.

Listing of Claims

1. (Currently Amended) A method for producing non-methylated DNA~~, wherein a~~ for use in methylation analysis ~~is used~~, comprising ~~the steps of~~:

a) performing a genome-wide amplification on genomic DNA[[,]] using non-methylated nucleotides or nucleotide triphosphates, thereby producing fully non-methylated DNA; and

b) using the amplificates generated in ~~step~~ a) as a non-methylated standard in the methylation analysis over a linear range.

2. (Canceled).

3. (Currently Amended) ~~A~~ The method of claim 1, wherein the amplification methods ~~performed are~~ is PEP, DOP-PCR or linker PCR.

4. (Currently Amended) ~~A~~ The method of claim 1, wherein the amplification method performed is a multiple displacement amplification (MDA).

5. (Currently Amended) ~~A~~ The method of claim 4, further comprising using a φ29-Polymerase.

6. (Currently Amended) ~~A~~ The method of claim 4, further comprising using a commercially available kit.

7. (Currently Amended) ~~A~~ The method of claim 6, wherein the commercially available kits are "GenomiPhi" (Amersham Biosciences) or "Repli-g" (Molecular Staging).

8. (Currently Amended) ~~A~~ The method of claim 4, further comprising a commercially available DNA produced by MDA is used as a standard.

9. (Currently Amended) ~~A~~ The method of claim 1, further comprising using restriction enzymes.

10. (Currently Amended) ~~A~~ The method of claim 1, further comprising performing the methylation analysis after conversion of the DNA into a form, in which methylated cytosines can be distinguished from non-methylated cytosines by means of hybridization, by methylation-specific ligation methods, MSP, Heavy Methyl or MethyLight.

11. (Currently Amended) ~~A~~ The method of claim 1, further comprising performing the methylation analysis after conversion of the DNA into a form, in which methylated cytosines can be distinguished from non-methylated cytosines by means of hybridization, by primer extension.

12. (Currently Amended) ~~A~~ The method of claim 1, further comprising performing the methylation analysis after conversion of the DNA into a form, in which methylated cytosines can be distinguished from non-methylated cytosines by means of hybridization, by an amplification and a hybridization of the amplificates at oligomer microarrays.

13. (Currently Amended) ~~A~~ The method of claim 1, further comprising performing the methylation analysis after conversion of the DNA into a form, in which methylated cytosines can be distinguished from non-methylated cytosines by means of hybridization, by means of a multiplex PCR.

14. (Currently Amended) ~~A~~ The method of claim 1, wherein ~~a mixture of methylated and~~ methylated DNA is mixed with the non-methylated DNA in a known amount to produce a mixture that is used as a standard.

15. (Currently Amended) ~~A~~ The methods of claim 1, wherein ~~several mixtures of methylated and~~ methylated DNA is mixed with the non-methylated DNA in known amounts to produce mixtures with different shares of methylated and non-methylated DNA that are used as ~~a~~ standards.

16. (Currently Amended) ~~A~~ The method of claim 1, wherein the methylation analysis is performed for the diagnosis of cancer diseases or other diseases associated with a modification of the methylation status.

17. (Currently Amended) ~~A~~ The method of claim 1, wherein the methylation analysis is performed for the prognosis of desired or undesired effects of drugs and for the differentiation of cell types or tissues, or for the investigation of the cell differentiation.

18-30. (Canceled).

31. (Currently Amended) ~~A~~ The method of claim 1, wherein the ~~genome-wide amplification is performed by exclusively using~~ non-methylated nucleotides or nucleotide triphosphates~~, respectively, which are non-methylated~~ are cytosine.

32-39. (Canceled).